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2508 #5

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RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/024,066

DATE: 05/02/2002
TIME: 14:18:08

Input Set : A:\IU-98us1.APP
Output Set: N:\CRF3\05022002\J024066.raw

ENTERED

3 <110> APPLICANT: Field, Loren J.
 4 Pasumarthi, Kishore Babu S.
 6 <120> TITLE OF INVENTION: CARDIOMYOCYTES WITH ENHANCED PROLIFERATIVE POTENTIAL,
 7 AND METHODS FOR PREPARING AND USING SAME
 9 <130> FILE REFERENCE: 7037-450
 11 <140> CURRENT APPLICATION NUMBER: 10/024,066
 12 <141> CURRENT FILING DATE: 2001-12-18
 14 <150> PRIOR APPLICATION NUMBER: 60/139,942
 15 <151> PRIOR FILING DATE: 1999-06-18
 17 <150> PRIOR APPLICATION NUMBER: PCT/US00/16827
 18 <151> PRIOR FILING DATE: 2000-06-19
 20 <160> NUMBER OF SEQ ID NOS: 8
 22 <170> SOFTWARE: PatentIn Ver. 2.1
 24 <210> SEQ ID NO: 1
 25 <211> LENGTH: 876
 26 <212> TYPE: DNA
 27 <213> ORGANISM: Mus musculus
 29 <220> FEATURE:
 30 <221> NAME/KEY: CDS
 31 <222> LOCATION: (4)..(870)
 33 <400> SEQUENCE: 1
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 35 Met Glu Leu Leu Cys Cys Glu Val Asp Pro Val Arg Arg Ala Val
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 38 ccg gac cgc aac ctg ctg gaa gac cgc gtt ctg cag aac ctg ttg acc 96
 39 Pro Asp Arg Asn Leu Leu Glu Asp Arg Val Leu Gln Asn Leu Leu Thr
 40 20 25 30
 42 atc gag gag cgc tac ctc ccg cag tgt tcc tat ttc aag tgc gtg cag 144
 43 Ile Glu Glu Arg Tyr Leu Pro Gln Cys Ser Tyr Phe Lys Cys Val Gln
 44 35 40 45
 46 aag gac atc caa ccg tac atg cgc agg atg gtg gcc acc tgg atg cta 192
 47 Lys Asp Ile Gln Pro Tyr Met Arg Arg Met Val Ala Thr Trp Met Leu
 48 50 55 60
 50 gag gtc tgt gag gaa caa aag tgt gaa gaa gag gtc ttt cct ctg gcc 240
 51 Glu Val Cys Glu Glu Gln Lys Cys Glu Glu Val Phe Pro Leu Ala
 52 65 70 75
 54 atg aat tac ctg gac cgt ttc ttg gct gga gtc ccg act cct aag acc 288
 55 Met Asn Tyr Leu Asp Arg Phe Leu Ala Gly Val Pro Thr Pro Lys Thr
 56 80 85 90 95
 58 cat ctt cag ctc ctg ggt gca gtg tgc atg ttc cta gct tcc aag ctg 336
 59 His Leu Gln Leu Leu Gly Ala Val Cys Met Phe Leu Ala Ser Lys Leu
 60 100 105 110
 62 aaa gag acc atc ccg ctg act gcg gaa aag ctg tgc att tac acc gac 384

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|-----|-------|------------|--------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 63 | Lys | Glu | Thr | Ile | Pro | Leu | Thr | Ala | Glu | Lys | Leu | Cys | Ile | Tyr | Thr | Asp | |
| 64 | | 115 | | | | 120 | | | | | | | 125 | | | | |
| 66 | aac | tct | gtg | aag | ccc | cag | gag | ctg | ctg | gag | tgg | gaa | ctg | gta | gtg | ttg | 432 |
| 67 | Asn | Ser | Val | Lys | Pro | Gln | Glu | Leu | Leu | Glu | Trp | Glu | Leu | Val | Val | Leu | |
| 68 | | | 130 | | | | | 135 | | | | | 140 | | | | |
| 70 | ggt | aag | ctg | aag | tgg | aac | ctg | gcc | gca | gtc | acc | cct | cac | gac | ttc | att | 480 |
| 71 | Gly | Lys | Leu | Lys | Trp | Asn | Leu | Ala | Ala | Val | Thr | Pro | His | Asp | Phe | Ile | |
| 72 | | 145 | | | | | 150 | | | | 155 | | | | | | |
| 74 | gag | cac | atc | ctt | cgc | aag | ctg | ccc | cag | caa | aag | gag | aag | ctg | tcc | ctg | 528 |
| 75 | Glu | His | Ile | Leu | Arg | Lys | Leu | Pro | Gln | Gln | Lys | Glu | Lys | Leu | Ser | Leu | |
| 76 | 160 | | | 165 | | | | | | 170 | | | | 175 | | | |
| 78 | atc | cgc | aag | cat | gcg | cag | acc | tcc | atc | gtc | ctg | tgc | gct | acc | gac | ttc | 576 |
| 79 | Ile | Arg | Lys | His | Ala | Gln | Thr | Phe | Ile | Ala | Leu | Cys | Ala | Thr | Asp | Phe | |
| 80 | | | | | 180 | | | | 185 | | | | 190 | | | | |
| 82 | aag | ttt | gcc | atg | tac | ccg | cca | tcg | atg | att | gca | act | gga | agc | gtg | gga | 624 |
| 83 | Lys | Phe | Ala | Met | Tyr | Pro | Pro | Ser | Met | Ile | Ala | Thr | Gly | Ser | Val | Gly | |
| 84 | | | | 195 | | | | | 200 | | | | 205 | | | | |
| 86 | gca | gcc | atc | tgt | ggg | ctt | cag | cag | gat | gat | gaa | gtg | aac | aca | ctc | acg | 672 |
| 87 | Ala | Ala | Ile | Cys | Gly | Leu | Gln | Gln | Asp | Asp | Glu | Val | Asn | Thr | Leu | Thr | |
| 88 | | | | | | 210 | | 215 | | | 220 | | | | | | |
| 90 | tgt | gat | gcc | ctg | act | gag | ctg | gtc | aag | atc | acc | cac | act | gat | gtg | | 720 |
| 91 | Cys | Asp | Ala | Leu | Thr | Glu | Leu | Leu | Ala | Lys | Ile | Thr | His | Thr | Asp | Val | |
| 92 | | | | 225 | | | 230 | | | 235 | | | | | | | |
| 94 | gat | tgt | ctc | aaa | gcc | tgc | cag | gag | caa | atc | gaa | gct | ctg | ctg | ctg | aac | 768 |
| 95 | Asp | Cys | Leu | Lys | Ala | Cys | Gln | Glu | Gln | Ile | Glu | Ala | Leu | Leu | Leu | Asn | |
| 96 | 240 | | | | 245 | | | | | 250 | | | 255 | | | | |
| 98 | agc | ctg | cag | cag | tcc | cgt | caa | gag | cag | cat | aac | gcc | gga | tcc | aag | tct | 816 |
| 99 | Ser | Leu | Gln | Gln | Phe | Arg | Gln | Glu | Gln | His | Asn | Ala | Gly | Ser | Lys | Ser | |
| 100 | | | | | 260 | | | 265 | | | 270 | | | | | | |
| 102 | gtg | gaa | gat | ccg | gac | caa | gcc | acc | acc | cct | aca | gac | gtg | cgg | gat | gtt | 864 |
| 103 | Val | Glu | Asp | Pro | Asp | Gln | Ala | Thr | Thr | Pro | Thr | Asp | Val | Arg | Asp | Val | |
| 104 | | | | 275 | | | | 280 | | | 285 | | | | | | |
| 106 | gac | ctg | tgagga | | | | | | | | | | | | | 876 | |
| 107 | Asp | Leu | | | | | | | | | | | | | | | |
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| 111 | <211> | LENGTH: | 289 | | | | | | | | | | | | | | |
| 112 | <212> | TYPE: | PRT | | | | | | | | | | | | | | |
| 113 | <213> | ORGANISM: | Mus musculus | | | | | | | | | | | | | | |
| 115 | <400> | SEQUENCE: | 2 | | | | | | | | | | | | | | |
| 116 | Met | Glu | Leu | Leu | Cys | Cys | Glu | Val | Asp | Pro | Val | Arg | Arg | Ala | Val | Pro | |
| 117 | 1 | | | | 5 | | | | | 10 | | | 15 | | | | |
| 119 | Asp | Arg | Asn | Leu | Leu | Glu | Asp | Arg | Val | Leu | Gln | Asn | Leu | Leu | Thr | Ile | |
| 120 | | | | 20 | | | | | 25 | | | 30 | | | | | |
| 122 | Glu | Glu | Arg | Tyr | Leu | Pro | Gln | Cys | Ser | Tyr | Phe | Lys | Cys | Val | Gln | Lys | |
| 123 | | | | | 35 | | | 40 | | | | 45 | | | | | |
| 125 | Asp | Ile | Gln | Pro | Tyr | Met | Arg | Arg | Met | Val | Ala | Thr | Trp | Met | Leu | Glu | |
| 126 | | | | 50 | | | | 55 | | | 60 | | | | | | |
| 128 | Val | Cys | Glu | Glu | Gln | Lys | Cys | Glu | Glu | Glu | Val | Phe | Pro | Leu | Ala | Met | |
| 129 | | | | | 65 | | | 70 | | | 75 | | | 80 | | | |

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131 Asn Tyr Leu Asp Arg Phe Leu Ala Gly Val Pro Thr Pro Lys Thr His
132             85          90          95
134 Leu Gln Leu Leu Gly Ala Val Cys Met Phe Leu Ala Ser Lys Leu Lys
135             100         105         110
137 Glu Thr Ile Pro Leu Thr Ala Glu Lys Leu Cys Ile Tyr Thr Asp Asn
138             115         120         125
140 Ser Val Lys Pro Gln Glu Leu Leu Glu Trp Glu Leu Val Val Leu Gly
141             130         135         140
143 Lys Leu Lys Trp Asn Leu Ala Ala Val Thr Pro His Asp Phe Ile Glu
144             145         150         155         160
146 His Ile Leu Arg Lys Leu Pro Gln Gln Lys Glu Lys Leu Ser Leu Ile
147             165         170         175
149 Arg Lys His Ala Gln Thr Phe Ile Ala Leu Cys Ala Thr Asp Phe Lys
150             180         185         190
152 Phe Ala Met Tyr Pro Pro Ser Met Ile Ala Thr Gly Ser Val Gly Ala
153             195         200         205
155 Ala Ile Cys Gly Leu Gln Gln Asp Asp Glu Val Asn Thr Leu Thr Cys
156             210         215         220
158 Asp Ala Leu Thr Glu Leu Leu Ala Lys Ile Thr His Thr Asp Val Asp
159             225         230         235         240
161 Cys Leu Lys Ala Cys Gln Glu Gln Ile Glu Ala Leu Leu Leu Asn Ser
162             245         250         255
164 Leu Gln Gln Phe Arg Gln Glu Gln His Asn Ala Gly Ser Lys Ser Val
165             260         265         270
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168             275         280         285
170 Leu
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177 <212> TYPE: DNA
178 <213> ORGANISM: Homo sapiens
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182 <222> LOCATION: (4)..(870)
184 <400> SEQUENCE: 3
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189 cgg gac cgc aac ctg ctc cga gac gac cgc gtc ctg cag aac ctg ctc      96
190 Arg Asp Arg Asn Leu Leu Arg Asp Asp Arg Val Leu Gln Asn Leu Leu
191             20          25          30
193 acc atc gag gag cgc tac ctt ccg cag tgc tcc tac ttc aag tgc gtg      144
194 Thr Ile Glu Glu Arg Tyr Leu Pro Gln Cys Ser Tyr Phe Lys Cys Val
195             35          40          45
197 cag aag gac atc caa ccc tac atg cgc aga atg gtg gcc acc tgg atg      192
198 Gln Lys Asp Ile Gln Pro Tyr Met Arg Arg Met Val Ala Thr Trp Met
199             50          55          60
201 ctg gag gtc tgt gag gaa cag tgc gaa gaa gag gtc ttc cct ctg      240
202 Leu Glu Val Cys Glu Gln Lys Cys Glu Glu Val Phe Pro Leu

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| 205 | gcc atg aat tac ctg gac cgt ttc ttg gct ggg gtc ccg act ccg aag | | | 288 |
| 206 | Ala Met Asn Tyr Leu Asp Arg Phe Leu Ala Gly Val Pro Thr Pro Lys | | | |
| 207 | 80 | 85 | 90 | .95 |
| 209 | tcc cat ctg caa ctc ctg ggt gct gtc atg ttc ctg gcc tcc aaa | | | 336 |
| 210 | Ser His Leu Gln Leu Leu Gly Ala Val Cys Met Phe Leu Ala Ser Lys | | | |
| 211 | 100 | 105 | 110 | |
| 213 | ctc aaa gag acc agc ccg ctg acc gcg gag aag ctg tgc att tac acc | | | 384 |
| 214 | Leu Lys Glu Thr Ser Pro Leu Thr Ala Glu Lys Leu Cys Ile Tyr Thr | | | |
| 215 | 115 | 120 | 125 | |
| 217 | gac aac tcc atc aag cct cag gag ctg ctg gag tgg gaa ctg gtg gtg | | | 432 |
| 218 | Asp Asn Ser Ile Lys Pro Gln Glu Leu Leu Glu Trp Glu Leu Val Val | | | |
| 219 | 130 | 135 | 140 | |
| 221 | ctg ggg aag ttg aag tgg aac ctg gca gct gtc act cct cat gac ttc | | | 480 |
| 222 | Leu Gly Lys Leu Lys Trp Asn Leu Ala Ala Val Thr Pro His Asp Phe | | | |
| 223 | 145 | 150 | 155 | |
| 225 | att gag cac atc ttg cgc aag ctg ccc cag cag cggtt ggg aag ctg tct | | | 528 |
| 226 | Ile Glu His Ile Leu Arg Lys Leu Pro Gln Gln Arg Glu Lys Leu Ser | | | |
| 227 | 160 | 165 | 170 | 175 |
| 229 | ctg atc cgc aag cat gct cag acc ttc att gct ctg tgt gcc acc gac | | | 576 |
| 230 | Leu Ile Arg Lys His Ala Gln Thr Phe Ile Ala Leu Cys Ala Thr Asp | | | |
| 231 | 180 | 185 | 190 | |
| 233 | ttt aag ttt gcc atg tac cca ccg tcg atg atc gca act gga agt gtg | | | 624 |
| 234 | Phe Lys Phe Ala Met Tyr Pro Pro Ser Met Ile Ala Thr Gly Ser Val | | | |
| 235 | 195 | 200 | 205 | |
| 237 | gga gca gcc atc tgt ggg ctc cag cag gat gag gaa gtg agc tcg ctc | | | 672 |
| 238 | Gly Ala Ala Cys Gly Leu Gln Gln Asp Glu Glu Val Ser Ser Leu | | | |
| 239 | 210 | 215 | 220 | |
| 241 | act tgt gat gcc ctg act gag ctg ctg gct aag atc acc aac aca gac | | | 720 |
| 242 | Thr Cys Asp Ala Leu Thr Glu Leu Leu Ala Lys Ile Thr Asn Thr Asp | | | |
| 243 | 225 | 230 | 235 | |
| 245 | gtg gat tgt ctc aaa gct tgc cag gag cag att gag gcg gtg ctc ctc | | | 768 |
| 246 | Val Asp Cys Leu Lys Ala Cys Gln Glu Gln Ile Glu Ala Val Leu Leu | | | |
| 247 | 240 | 245 | 250 | 255 |
| 249 | aat agc ctg cag cag tac cgt cag gac caa cgt gac gga tcc aag tcg | | | 816 |
| 250 | Asn Ser Leu Gln Gln Tyr Arg Gln Asp Gln Arg Asp Gly Ser Lys Ser | | | |
| 251 | 260 | 265 | 270 | |
| 253 | gag gat gaa ctg gac caa gcc agc acc cct aca gac gtg cgg gat atc | | | 864 |
| 254 | Glu Asp Glu Leu Asp Gln Ala Ser Thr Pro Thr Asp Val Arg Asp Ile | | | |
| 255 | 275 | 280 | 285 | |
| 257 | gac ctg tga | | | 873 |
| 258 | Asp Leu | | | |
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| 262 | <211> LENGTH: 289 | | | |
| 263 | <212> TYPE: PRT | | | |
| 264 | <213> ORGANISM: Homo sapiens | | | |
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| 267 | Met Glu Leu Leu Cys His Glu Val Asp Pro Val Arg Arg Ala Val Arg | | | |
| 268 | 1 | 5 | 10 | 15 |

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270 Asp Arg Asn Leu Leu Arg Asp Asp Arg Val Leu Gln Asn Leu Leu Thr
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 273 Ile Glu Glu Arg Tyr Leu Pro Gln Cys Ser Tyr Phe Lys Cys Val Gln
 274 35 40 45
 276 Lys Asp Ile Gln Pro Tyr Met Arg Arg Met Val Ala Thr Trp Met Leu
 277 50 55 60
 279 Glu Val Cys Glu Glu Gln Lys Cys Glu Glu Val Phe Pro Leu Ala
 280 65 70 75 80
 282 Met Asn Tyr Leu Asp Arg Phe Leu Ala Gly Val Pro Thr Pro Lys Ser
 283 85 90 95
 285 His Leu Gln Leu Leu Gly Ala Val Cys Met Phe Leu Ala Ser Lys Leu
 286 100 105 110
 288 Lys Glu Thr Ser Pro Leu Thr Ala Glu Lys Leu Cys Ile Tyr Thr Asp
 289 115 120 125
 291 Asn Ser Ile Lys Pro Gln Glu Leu Leu Glu Trp Glu Leu Val Val Leu
 292 130 135 140
 294 Gly Lys Leu Lys Trp Asn Leu Ala Ala Val Thr Pro His Asp Phe Ile
 295 145 150 155 160
 297 Glu His Ile Leu Arg Lys Leu Pro Gln Gln Arg Glu Lys Leu Ser Leu
 298 165 170 175
 300 Ile Arg Lys His Ala Gln Thr Phe Ile Ala Leu Cys Ala Thr Asp Phe
 301 180 185 190
 303 Lys Phe Ala Met Tyr Pro Pro Ser Met Ile Ala Thr Gly Ser Val Gly
 304 195 200 205
 306 Ala Ala Ile Cys Gly Leu Gln Gln Asp Glu Glu Val Ser Ser Leu Thr
 307 210 215 220
 309 Cys Asp Ala Leu Thr Glu Leu Leu Ala Lys Ile Thr Asn Thr Asp Val
 310 225 230 235 240
 312 Asp Cys Leu Lys Ala Cys Gln Glu Gln Ile Glu Ala Val Leu Leu Asn
 313 245 250 255
 315 Ser Leu Gln Gln Tyr Arg Gln Asp Gln Arg Asp Gly Ser Lys Ser Glu
 316 260 265 270
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 321 Leu
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 334 ttcaaaaagg g cctgaatgag gagtagatct tttgttaccc agctctaagg gtgcccgtga 180
 335 agccctcaga cctggagcct ttgcaacagc cctttaggtg gaagcagaat aaagcaattt 240
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 337 agggtggggaa ggtggggctt ggaagaagaa ggtggggaaag tggcaaaagc cgatccctag 360
 338 ggcctgtga agttcggagc ctccctgtt cagcactggc tcata gatcc tcctccagcc 420
 339 aaacatagca agaagt gata cctccctt gacttccccca gccc cagttac ctgtcaggtt 480
 340 gaaacaggat tttagagaagc ctctgaactc acctgaactc tgaagctcat ccaccaagca 540

VERIFICATION SUMMARY

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